

Agilent 5100 Automated Lab-on-a-Chip Platform

DNA 1000HT⁴ Quick Start Guide



Edition July 2004



Agilent Technologies

Notices

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Software Revision

This guide is valid for A.01.xx revisions of the Agilent 5100 Automated Lab-on-a-Chip Platform software, where xx refers to minor revisions of the software that do not affect the technical accuracy of this guide.

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WARNING

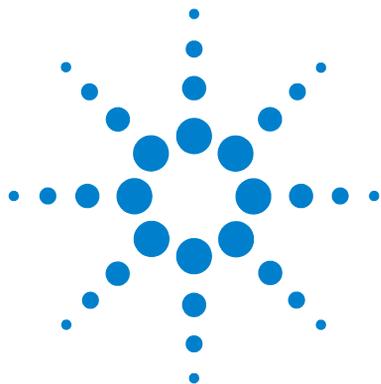
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Manual Title Variable

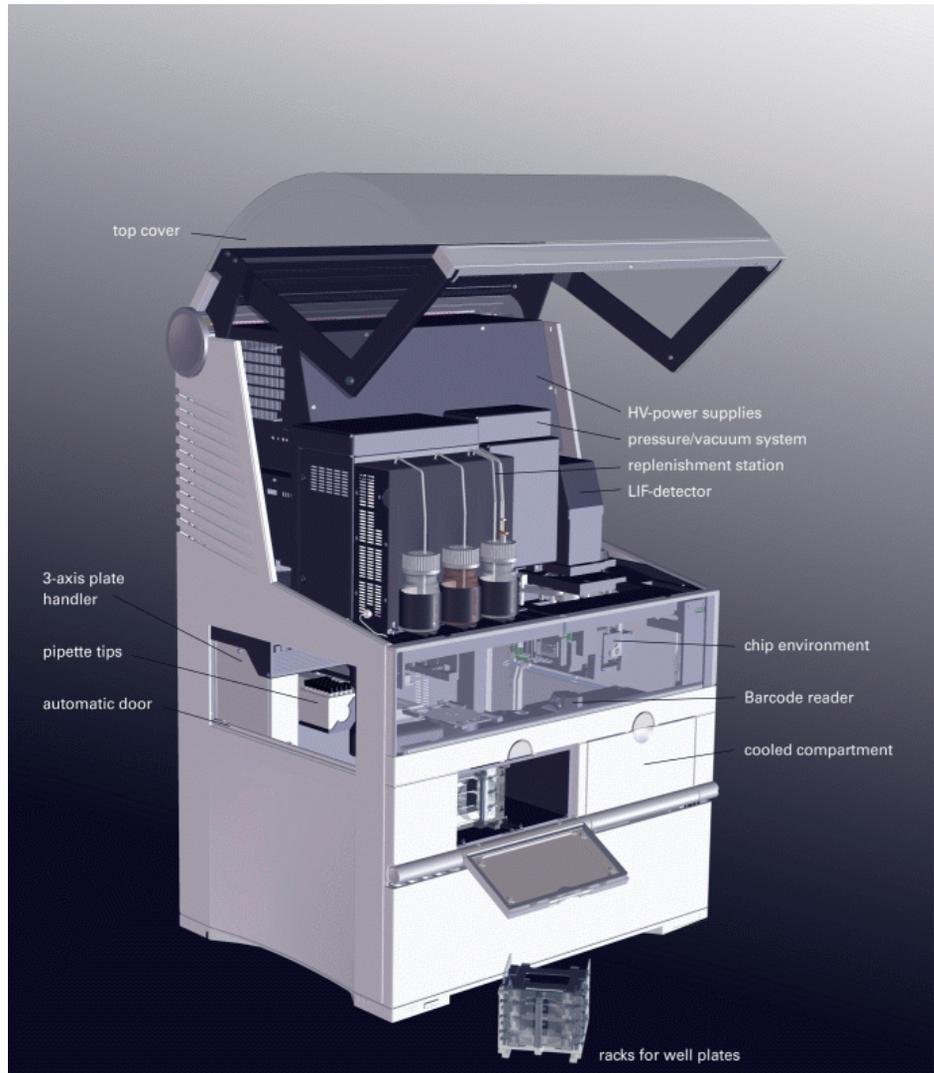


5100 ALP DNA1000-HT- Quick Start Guide

This quickstart guide will introduce you to the basics of DNA analysis using the Agilent 5100 Automated Lab-on-a-chip Platform (ALP). It will give you a short overview on the hardware and software and will guide you through a standard process of analyzing your DNA samples.



ALP instrument

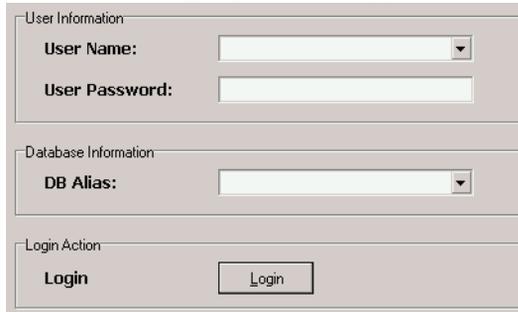


Log on to the 5100 ALP software

- 1 Switch on the ALP PC-Server and instrument and wait one minute until the system is initialized
- 2 Go to your desktop and double-click the following icon:



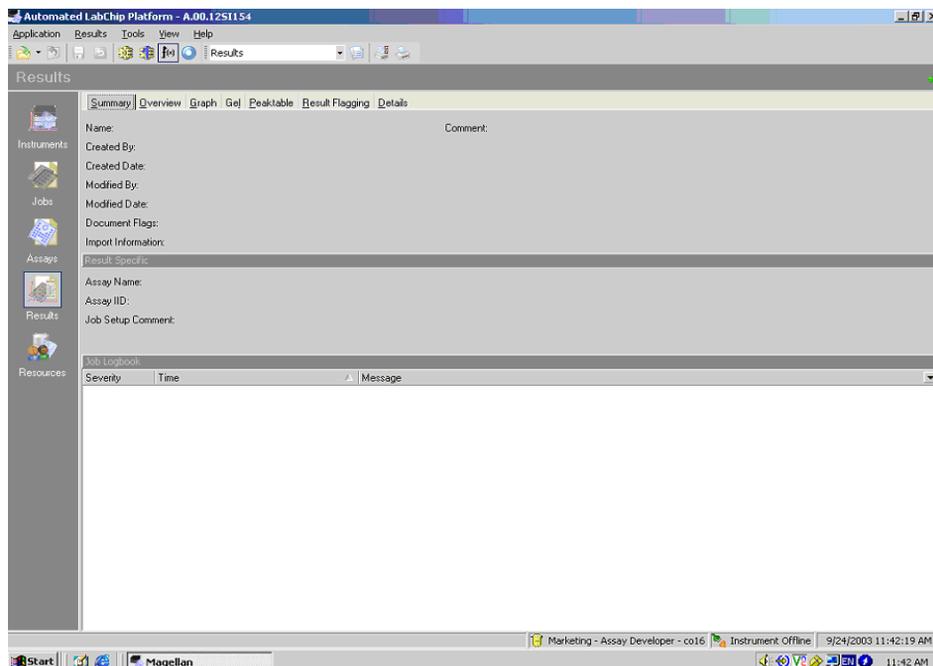
- 3 The following login screen appears:

A screenshot of a login window with a light gray background and a thin border. The window is divided into three sections. The top section is titled "User Information" and contains two fields: "User Name:" followed by a white text box with a small downward arrow on the right, and "User Password:" followed by a white text box. The middle section is titled "Database Information" and contains one field: "DB Alias:" followed by a white text box with a small downward arrow on the right. The bottom section is titled "Login Action" and contains a "Login" label on the left and a "Login" button on the right. The button is a small rectangle with a thin border and the word "Login" inside.

- 4 In order to get access to the software you need to provide login information. Type in your user name and user password and select the appropriate database alias from the drop down menu. Click on the Login button and the main screen of the software appears as follows:

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Log on to the 5100 ALP software



The 5100 ALP software is organized in contexts. The icons on the left column of the screen provide access to different contexts within the software:

Instruments:

This context is used to:

- connect to the instrument,
- start a job,
- display the incoming signal traces,
- check the instrument status.

Jobs:

This context is used to set-up an experiment (job) on ALP. Each job is based on an assay, which defines the internal instrument control and setpoints for data acquisition. For example the DNA 1000 HT4 assay is used for the analysis of DNA samples.

A job contains the following information, which must be entered before the execution of a job:

- assay, e.g. HT DNA 1000, which compromise set points for data acquisition and evaluation
- the number and type of well plates that are processed during the job
- storage position of the well plates inside the instrument
- barcode information of the well plates
- the position of samples on each well plate and sample names
- optional: rules for result flagging
- required resources and instrument configuration

After job execution, it contains sample and ladder data that is stored in the database.

For the analysis of DNA samples on ALP, either a new job has to be defined or an already existing job in the database could be opened as a job copy.

After completing the analysis, the results can be reviewed in the Results context. For this the operator has to switch to the Results context.

Results: This context allows the user to get detailed information about the results of the analysis. The results context shows the acquired data both as electropherograms and gel like images, whereas the calculated values (e.g. concentration, fragment size, molarity) are listed in peak tables. The software provides several different way to filter and organize the data.

If not previously done within the Job Setup this context can also be used to define result flagging rules after the data has been acquired.

NOTE

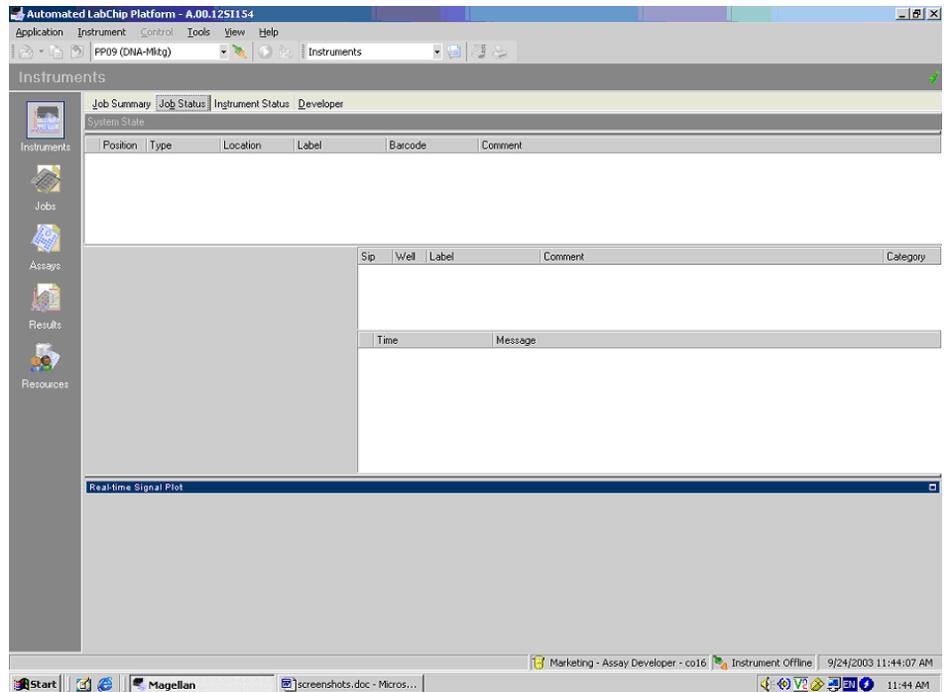
After login the appearance of the software depends on the last opened context.

Connecting to the instrument

NOTE

Make sure that the instrument is switched on and initialized.

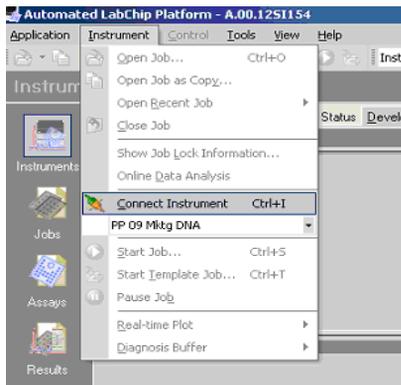
- 1 Click on Instruments to switch to the Instrument Context. The icon of the selected context will be highlighted on the Context menu of the 5100 ALP software:



2 In the software screen select the appropriate Instrument from the menu bar



3 Select the *Instrument* Menu bar and click the *Connect Instrument* button or click on the Connect Instrument button  in the menu bar to connect to the ALP instrument. When connection succeeded, the button will change to *Disconnect Instrument*.



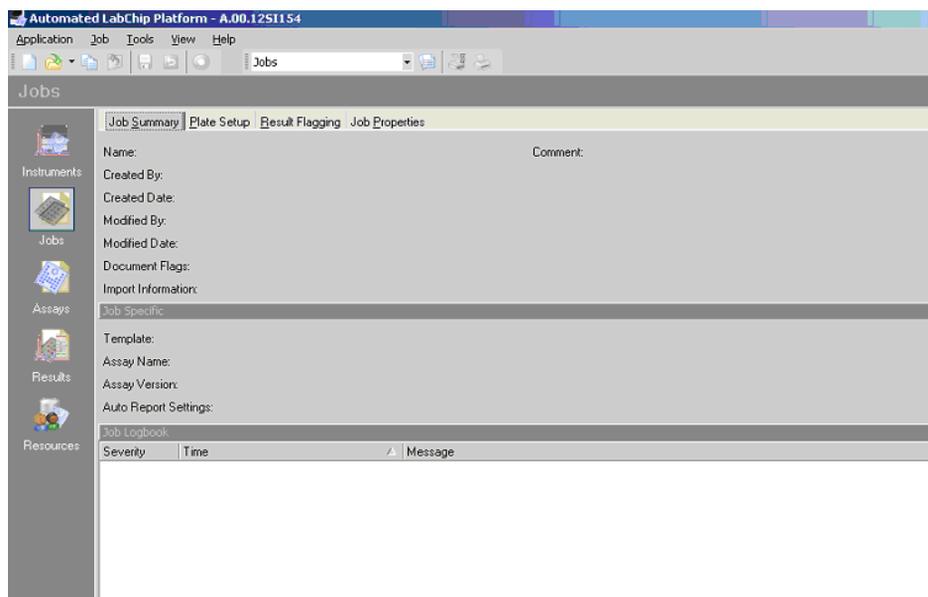
NOTE

After connection succeeded - the Real-time Signal Plot shows the online signal traces within the *Job-* and the *Instrument Status* tab.

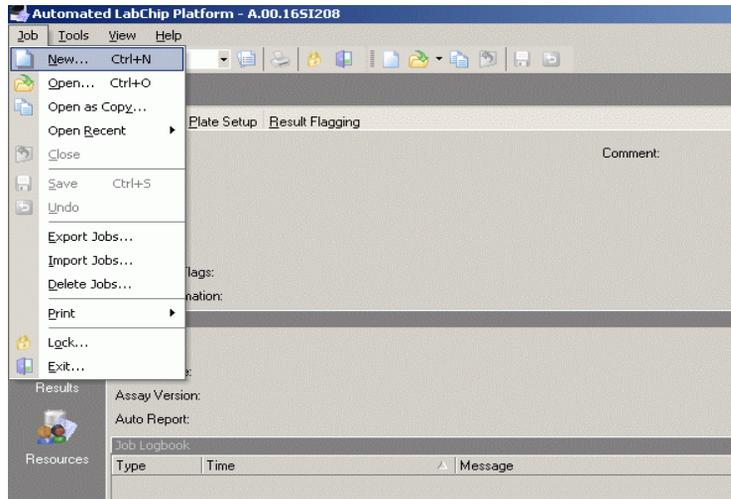
Creating a new Job

Before starting the measurement of DNA samples several experiment parameters must be defined within the 5100 ALP Software. To provide all important information to the instrument a new job must be created within the *Jobs* context. During the run-time execution a job comprises the control of the process flow of sample and ladder runs as well as the resource management of reagent, chips and pipette tips.

- 1 Click on the *Jobs* icon to switch to the Jobs Context. The icon of the selected context will be highlighted on the Context menu of the 5100 ALP software will appear:



- 2 To create a new job: Select the *Jobs* Menu bar. Select *New* and a new job will be opened.

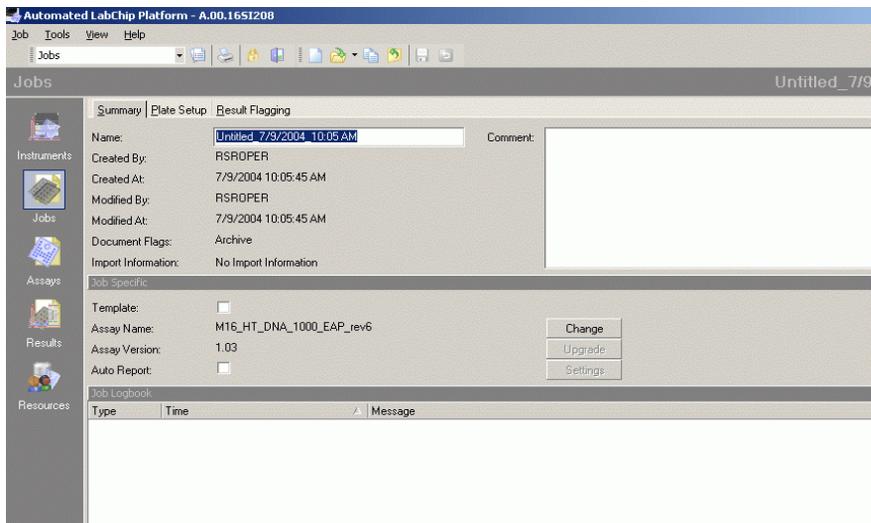


- 3 The Select Base Assay dialog box appears. For the measurement of DNA samples - Select the DNA 1000 Assay and click *Use Assay* to add the selected assay to the job. The name of the assay as well as the version will appear in the Job Summary tab

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Creating a new Job

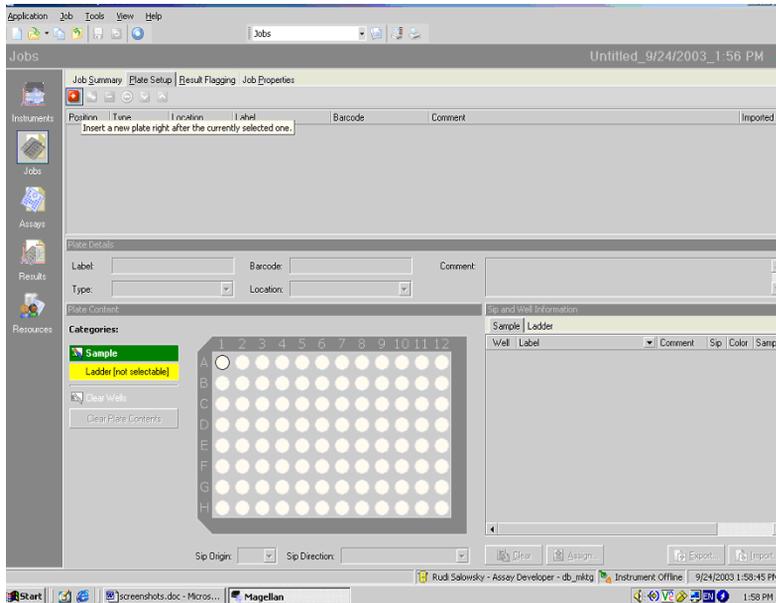
4 Enter a new job name and a comment in the *Summary* tab.



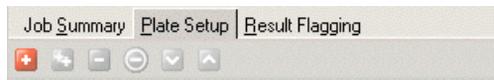
5 To setup the microtiter plates that should be analyzed during the job switch to Plate Setup tab. The Microtiter plate setup will define:

- the number of samples and their position on the sample plate
- the sample plate type
- the location of the sample plates within the storage compartment (Depot).

The plate Setup tab appears as follows:



6 Click on the red add-button  to add a sample plate to the plate list tab.



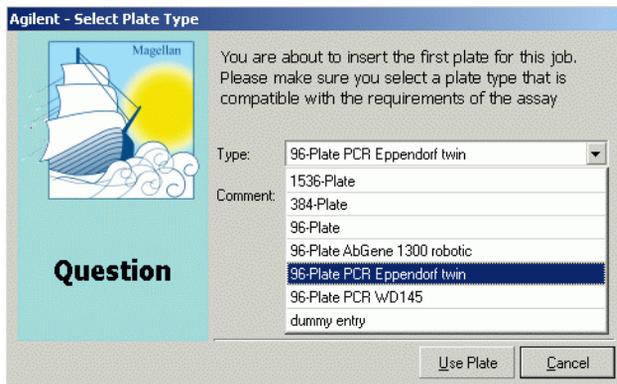
NOTE

One line in the Plate setup table represents one sample plate.

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Creating a new Job

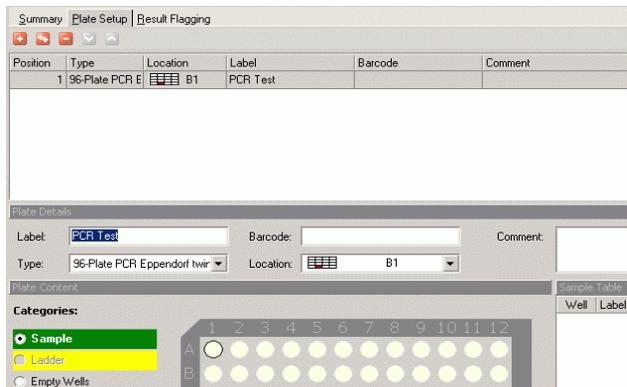
- 7 The *select plate type* dialog box appears. Select the sample plate type from the drop down menu.



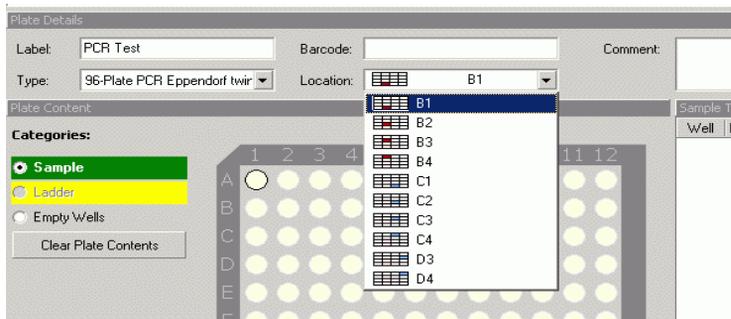
- 8 Press *Use Plate*.
- 9 The selected sample plate appears in the *Plate Setup* tab.

| Job Summary | | | | | |
|-----------------|-------------|--|---------|---------|---------|
| Plate Setup | | | | | |
| Result Flagging | | | | | |
| Position | Type | Location | Label | Barcode | Comment |
| 1 | *96PCR_EPDF |  B1 | Plate 1 | | |

10 Insert a label for the selected plate in the plate details section of the *Plate Setup* tab .



11 Select the location of the sample plate inside the Depot of the 5100 ALP instrument.



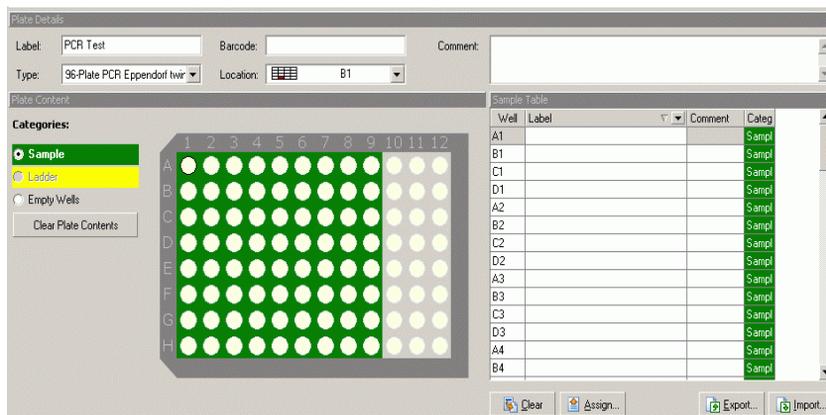
CAUTION

Using a rack applicable for the storage of only two plates - the lowest position is labelled with B1 followed by B2 for the upper position. Avoid the selection of positions B3 and B4 while using a two plate rack.

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Creating a new Job

12 To define the content of your sample plate drag the mouse over the wells of the microtiter plate on the screen. The selected wells appears green. By using a HT4-Sipper chip - always 4 samples will be processed in parallele and therefore 4 wells on the sample plate are always selected together. By selecting the wells the information will be directly submitted to the *Sample table* on the right side of the screen.



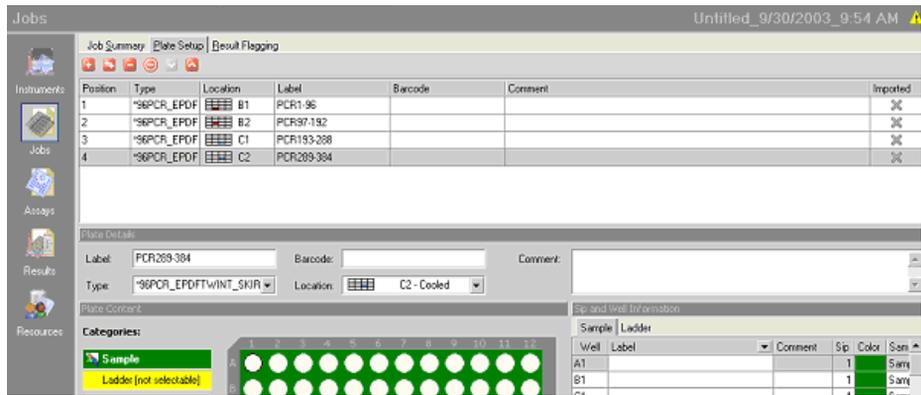
13 Click the red add-button to add further sample plates to the *Plate Setup* tab.

NOTE

The performance of the 5100 ALP instrument is optimized for the measurement of 4 x 96 well or 1 x 384 well sample plates.

NOTE

After defining 4 x 96 well plates - the Plate Setup tab should contain 4 lines representing all defined sample plates.



- 14 Select Job>Save to save the newly created job to the database.
- 15 Select Job>Close to close the newly created job in the *Jobs* context.
- 16 To start a job on the 5100 ALP instrument switch to the *Instruments* context and open the job selected for analysis.

NOTE

Before opening a job in the Instrument context - the job must be closed in the Job context.

HT4 DNA Assay Protocol

Reagent, supplies and equipment supplied by Agilent:

HT4-DNA 1000 reagent and supplies (order number xxx)

HT⁴ DNA 1000 Reagents & Supplies

- HT⁴ DNA 1000 Storage buffer
- HT⁴ DNA 1000 Marker
- HT⁴ DNA Gel Matrix
- HT⁴ DNA Dye
- HT⁴ DNA focussing solution
- HT⁴ DNA Ladder (10x)
- Reagent plate
-

HT⁴ DNA Chip (order number xxx)

- HT⁴ Sipper Chip

additional material and equipment required:

- Pipettes (10 µl, 20 µl, 100 µl and 1000 µl) with compatible tips
- Deionized water
- microtiter-plate-centrifuge
- microtiter plate compatible PCR-machine with heatable lid
- high pressure connection
- microtiter plate sealer



Preparing the Reagent Plate

Before the analysis of DNA samples, the chip will automatically be filled with reagents by the ALP system. To provide all reagents for the chip replenishment, a reagent plate has to be prepared by the user and inserted in the dedicated depot position. One prepared column of the reagent plate should contain reagents (gel, gel-dye and marker) sufficient for the analysis of 384 samples (e.g. 1x 384 well plate or 4x96 well plates).

For the analysis of more than 384 samples the number of columns filled with reagents must be calculated and adjusted.

Preparing the Gel-Dye Mix

WARNING

Wear hand and eye protection and follow good laboratory practices when preparing and handling reagents and samples. Kit components contain DMSO. No data is available addressing the mutagenicity or toxicity of the dye/DMSO reagent. Because the dye binds to nucleic acids, it should be treated as a potential mutagen and used with appropriate care. The DMSO stock solutions should be handled with particular caution as DMSO is known to facilitate the entry of organic molecules into tissues.

1 Allow all reagent to equilibrate to room temperature for 30 minutes

NOTE

It is important that all reagents have room temperature before starting the next step. Protect the dye concentrate from light.



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HT4 DNA Assay Protocol

- 2 In a microcentrifuge tube, pipette 280 μ l of the DNA gel.
- 3 Vortex the DNA dye concentrate for 10 seconds and spin down.
- 4 Pipette 10.5 μ l of the dye concentrate (colour) to the tube with 280 μ l of the DNA gel.
- 5 Cap the tube, vortex for 10 seconds. Visually inspect proper mixing of gel and dye. Store the dye at 4°C in the dark again.
- 6 Transfer the gel-dye mix to the designated well position on the reagent plate (Refer to *Pipetting the Reagent Plate* on page 23)

NOTE

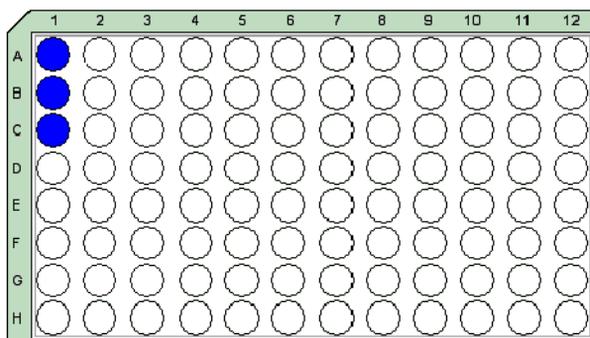
Use the gel-dye within 1 week of preparation. Protect the gel dye from light-the dye will degrade when exposed to light and this reduces signal intensity. Store the gel-dye mix at 4°C when not in use for more than 1 hour.

Pipetting the Reagent Plate

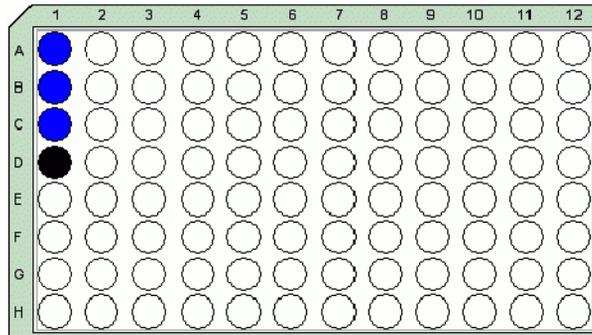
NOTE

Always fill reagents in unused columns on a reagent plate.

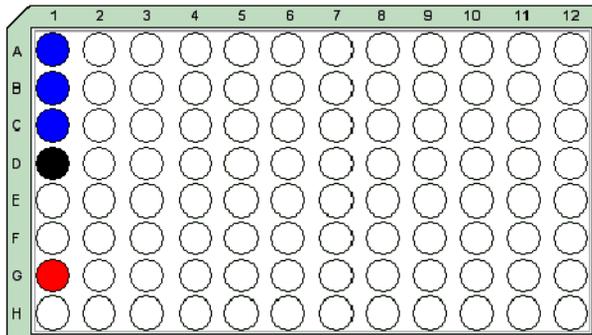
- 1 Pipette 250 μ l of the gel in each of the gel wells A1, B1 and C1 on the reagent plate.



2 Transfer 250 μ l of the gel-dye mix to the well D1 on the reagent plate.

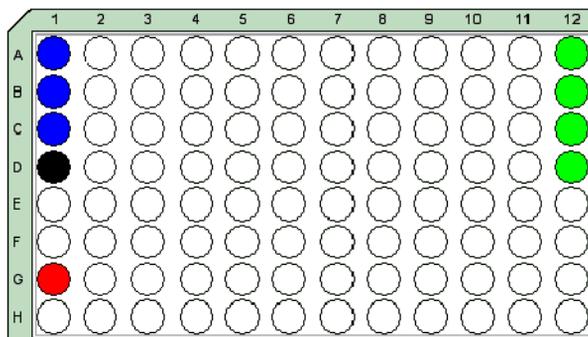


3 Pipette 300 μ l of the marker (red) to the well G1 on the reagent plate.



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HT4 DNA Assay Protocol

- 4 Pipette 250 µl of the focussing solution in each of the wells A12, B12, C12 and D12 on the reagent plate.



NOTE

For the analysis of more than 384 samples the number of columns filled with reagents has to be adjusted (e.g. 3 reagent columns for 3 x 384- or 12 x 96 well sample plates). The position of the prepared columns on the reagent plate must be entered in the Start Job execution dialog before starting a job (Refer to *Start Job Execution Dialog* on page 36.).

- 5 Seal the reagent plate with aluminum foil on the Remp plate sealer at 170°C for 4 seconds.
- 6 Place the reagent plate in the designated rack located in position D of the right depot. Column 1 of the reagent plate must face the handle of the rack and the Chip Tub must be held by the clamps of the rack.
- 7 Insert the rack into the depot. The position of the reagent plate in the depot will be shown in the Instrument Status tab of the Instrument context



Preparing the Sample Plate

The Agilent 5100 ALP system is able to analyze DNA samples prepared either on 96- or on a 384 well plate. DNA samples should be prepared according to the HT⁴ DNA1000 assay specifications.

- 1 Confirm that your 96- or 384 well sample plate was specified by Agilent as appropriate for the ALP system
- 2 Pipette at least 20 μ l of your samples on the designated wells of the sample plate

NOTE

The sample volume within each well should always exceed 25 μ l. Lower sample volumes may cause impaired analyses

- 3 Seal the sample plate with aluminum foil on the Remp plate sealer for 4 seconds at 170°C.
- 4 Place the sample plate in the designated rack. Column 1 of the sample plate must face the handle of the rack and the plate must be held by the clamps of the rack.
- 5 Insert the rack into the designated position of the depot as defined before in the Job Set-up.



Preparing the HT⁴ DNA 1000 Chip

The DNA1000 HT⁴ Chip will be shipped ready-to-use in a specific box filled with storage buffer.

CAUTION

Always place the chip in the Chip Carrier or in the designated storage box. The chip contains 4 sippers on the underside of the chip. The sippers are fragile capillaries that can easily be damaged if not handled with care.

- 1 Take the Chip Tub and the Chip Carrier out of the depot.

NOTE

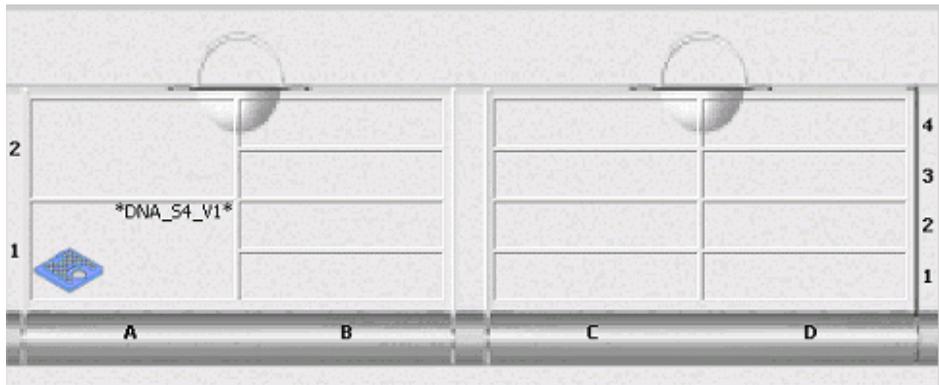
The Chip Carrier is the receptacle for the HT4DNA chip and is positioned on the Chip Tub.

- 2 Remove the Chip Carrier from the Chip Tub. Fill water in the water bath of the Chip Tub until the fins in tray well are covered with liquid.
- 3 Position the Chip Carrier on the Chip Tub.
- 4 Take the HT⁴ DNA Chip out of the Storage box. Remove the liquid from the underside of the chip.
- 5 Clean the detection window of the chip by filling it with iso-propanol.
- 6 Carefully remove the iso-propanol with a pipette and cover the detection window with water. Carefully remove the water with a pipette and let the detection window dry up.
- 7 Insert the chip into the Chip Carrier. The sippers must be inserted in the cut-out of the Chip Carrier.

CAUTION

The chip fits only one way. Do not force the chip insert. Otherwise capillaries may be damaged

- 8 Insert the Chip Tub with Chip Carrier and chip into the designated position of the rack. The electrodes of the Chip Carrier must face the handle of the rack and the Chip Tub must be held by the clamps of the rack.
- 9 Insert the rack into the depot. The position of the reagent plate in the depot will be shown in the Instrument Status tab of the Instrument context.



Preparing the Trough

The trough is a storage device for locating the DNA Ladder in the instrument. Before starting a job, the trough has to be manually filled with DNA Ladder and inserted in the ALP 5100 instrument.

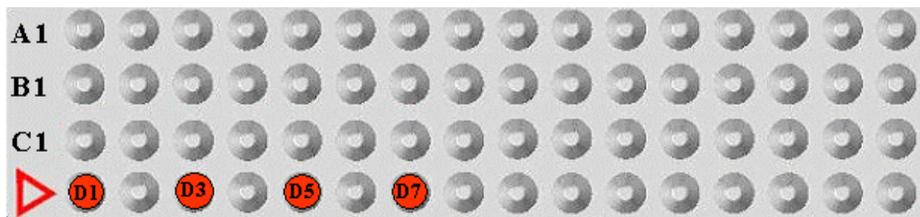
- 1 Dilute the 10 x DNA Ladder 1:10 to a final concentration of 1x DNA Ladder.

CAUTION

Ladder and DNA samples should always have the same salt concentration. Adjust the salt concentration of the ladder to the salt concentration of the DNA sample by diluting the 10 x DNA Ladder with sample buffer. Sample buffers as PCR- and Restriction enzyme buffers are often 10 x concentrated

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HT4 DNA Assay Protocol

- 2** For the analysis of 384 DNA samples (1 x 384- or 4 x 96 well plate) - fill 4 x 25 μ l of 1 x DNA Ladder in the trough wells starting with well positions D1, D3, D5, D7. The position D1 on the trough is marked by an arrow head and should be located down to the left.



CAUTION

Avoid air bubbles on the bottom of the wells while pipetting ladder to the trough. Visible bubbles within the Ladder must be removed before starting the analysis.

NOTE

For the analysis of a higher sample number - adjust the number of filled trough wells. Continue to fill wells with position D2, D4, D6, D8 of the trough and proceed in the filling procedure from the lower left to the upper right position of the trough.

- 3** Insert the trough in a 384 well plate. Seal the trough with aluminum foil on a Remp-plate sealer for 6 sec at 170°C and cut off the extending foil. The sealed trough can either be used directly for analysis (refer to Starting a Job - page 37) or stored at 4°C for maximum 7 days.

Starting a Job

- 1 Switch to the Instrument Context. The icon of the selected context will be highlighted on the Context menu of the 5100 ALP software.

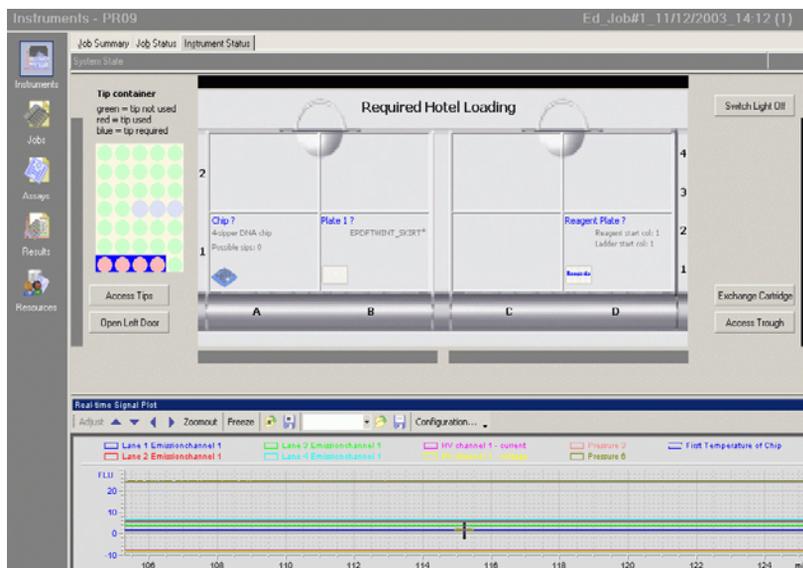
NOTE

Before starting a job - the Magellan Software has to be connected with the ALP 5100 instrument.

- 2 Go to Instrument>OpenJob and select a job. Click the *Open Job* button to open the selected Job.
- 3 The Instrument status tab shows an overview of the different hotel compartments of the instrument.

NOTE

At this point of job execution the Required Hotel Loading information shows the required position of chips, reagents and samples as defined by the selected Job.

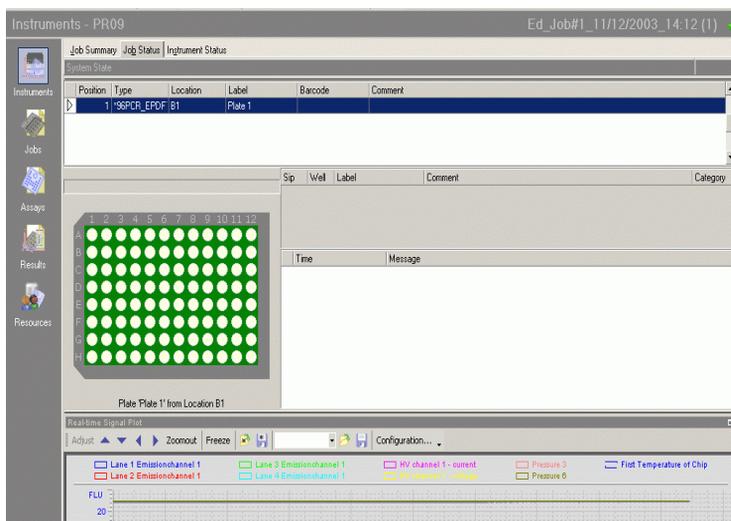


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Starting a Job

NOTE

The Job Status Tab provides information on the number and type of the sample plates as defined by the selected Job



4 Insert Chips, Reagent plates and sample plates as indicated by the *Required Hotel Loading* information within the *Instrument Status* tab.

CAUTION

Column 1 (including well A1) of both the reagent plate and the sample plates as well as the electrodes of the Chip must face the handle of their designated racks. Wrong Chip position impairs the instrument processes and may damage the chip. Wrong reagent- and sample plate positions will lead to inappropriate results and may destroy the chip.

5 Close all Hotel doors.

NOTE

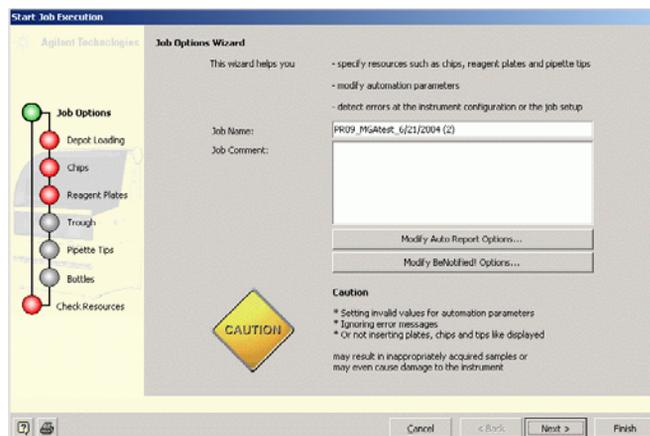
All instrument doors must be closed before starting a job. Executing a job with opened doors will lead to an instrument error

- 6 Click on Instrument>Start Job or on the *Execute Job* button on the menu bar to execute the selected job
- 7 The start Job Execution dialog appears.

Start Job Execution dialog

CAUTION

The Start Job execution dialog leads through a process of successive steps required to finalize the instrument preparation and to check the availability of all resources needed for a successful job execution. All topics have to be carefully checked by the operator before proceeding with the final job execution.



- 1 Click on *Next* to proceed with the Job Start execution dialog.

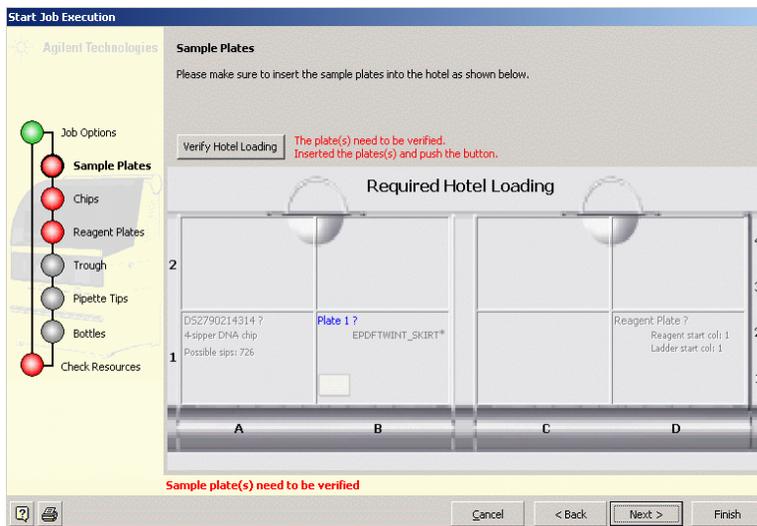
NOTE

Before verifying the loading of the depot, check the number of the column of the reagent plate prepared for chip replenishment.

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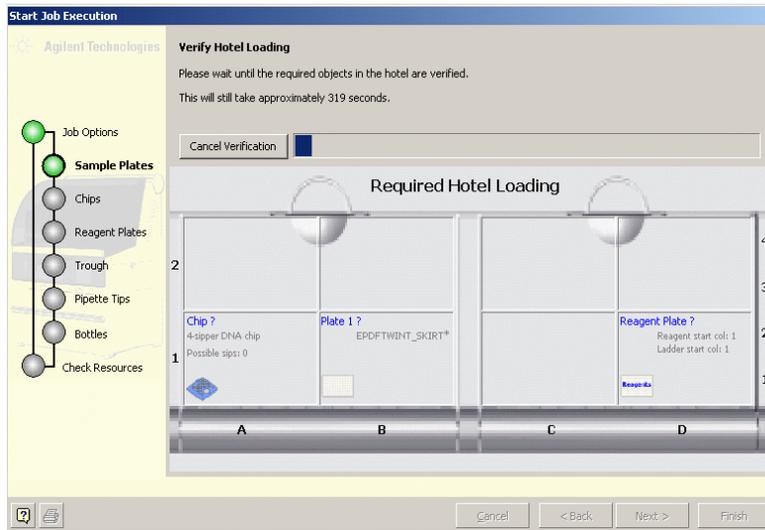
Starting a Job

- 2 Click on *Verify Hotel Loading* and the instrument will check the status of the hotel loading.



NOTE

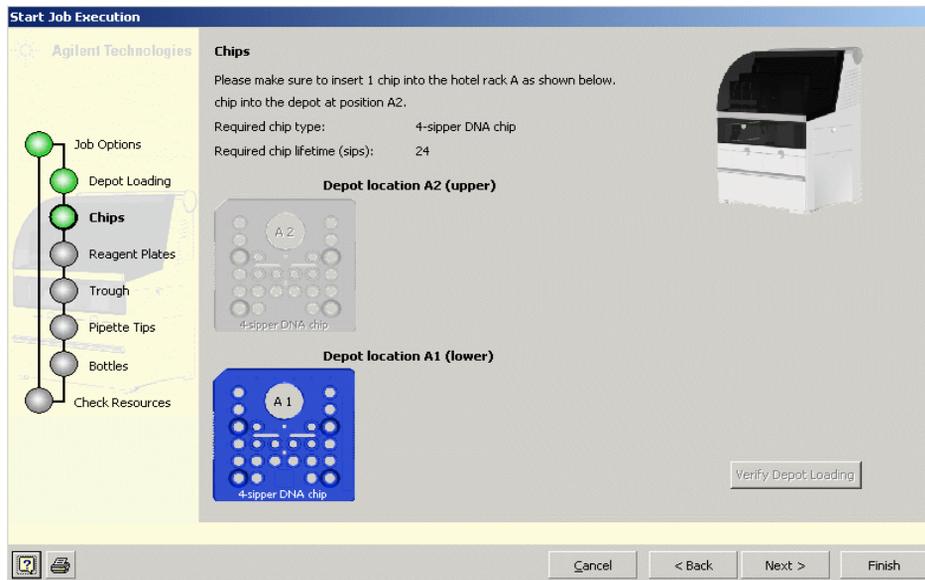
The instrument may need up to 5 minutes to verify the hotel loading. The subsequent opening of Hotel doors and exchange of plates will require a repeat of the hotel loading verification.



- 3 After completion of the Hotel Loading verification - click *Next* to proceed with the Job start execution dialog. The Job Start Execution dialog provides information on the identified chip.

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Starting a Job

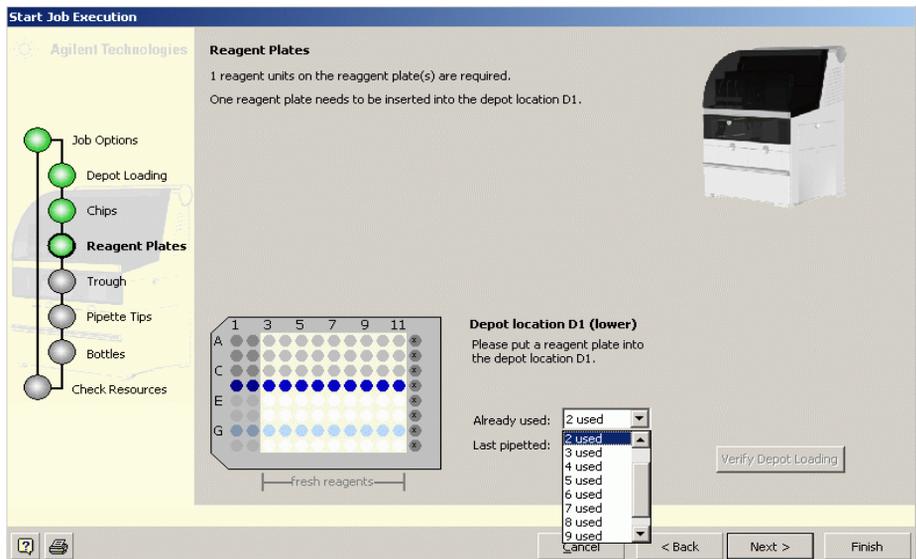


- 4 Click *Next* to proceed with the Job Start execution dialog.
- 5 Check the origin of your reagent plate. The first unused column filled with reagent has to be defined

NOTE

The reagent plate may contain reagent for several different jobs. The instrument needs the information on the position of prepared and unused reagent columns. The number of the first unused column on the reagent plate provides enough information to proceed.

- To define the column of prepared reagent selected for instrument preparation by inserting the number of used columns in the *Already Used* drop down menu.



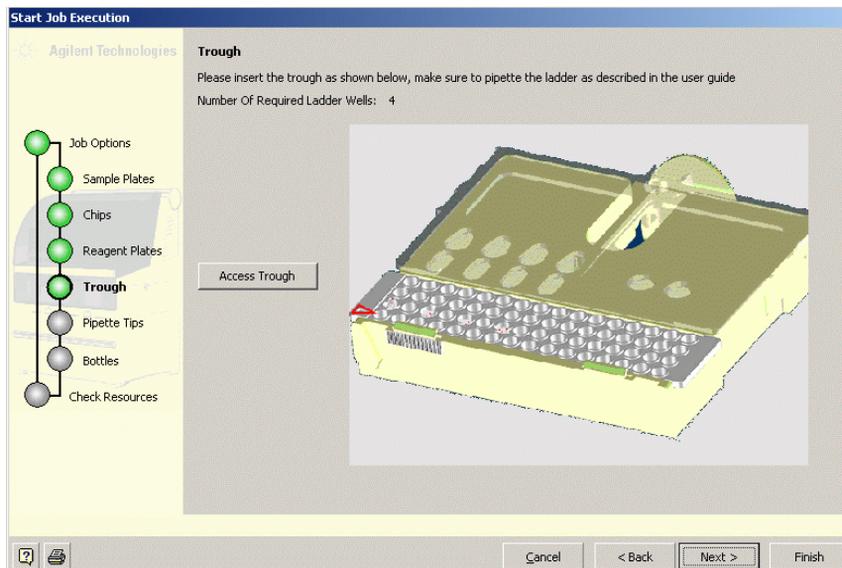
CAUTION

Inserting the number of a used or unprepared reagent plate column may damage the chip.

- Click next to proceed with the Job Start execution dialog.

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Starting a Job

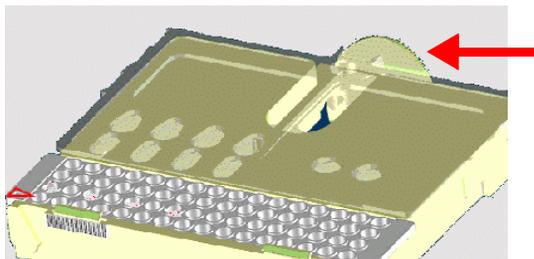


- 8 Click on *Access Trough* to insert a prepared Trough in the Trough Support.

NOTE

Wait until the plate handler was positioned below the right backside door and the instrument was inactive for at least 10 seconds.

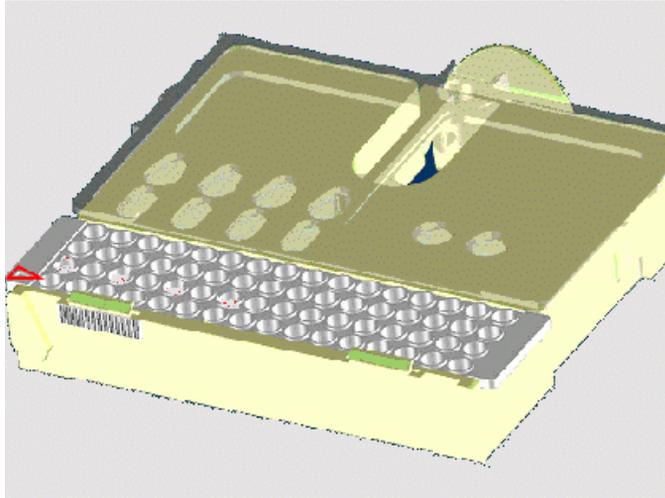
- 9 Manually open the right door. Press the clip on the back of the Trough Support to remove it from the plate handler.



NOTE

Remove used Ladder Troughs from the Trough Support. Do not use Ladder Troughs twice.

10 Insert the trough into the Trough Support as follows:



NOTE

The arrow head on trough must be located at the lower left corner of the trough support. The trough fits only one way.

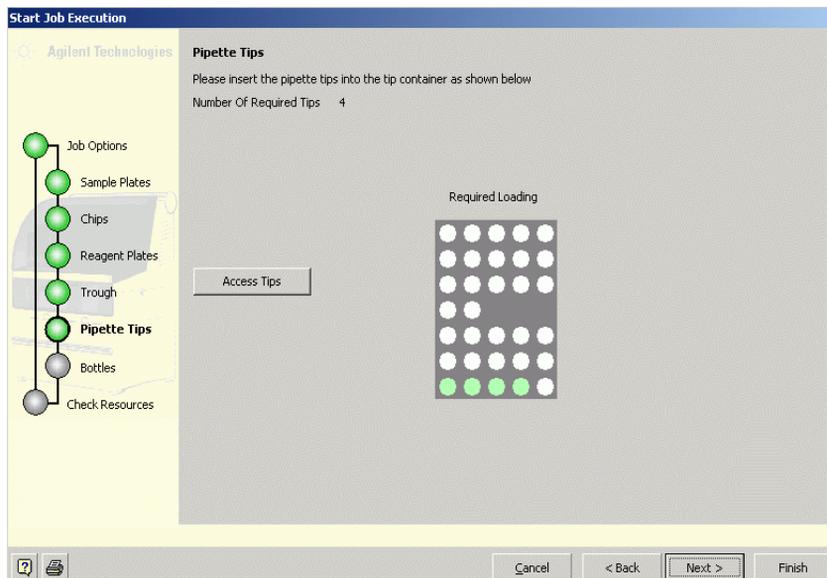
11 Insert the Trough Support with trough in the designated position of the plate handler. The lock of the latch will click when Trough Support is inserted correctly.

12 Manually close the right door.

13 Click next to proceed with the Job Start execution dialog.

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Starting a Job



14 Click on **Access Tips** to insert new tips into the tip container. The left door will be automatically opened by the instrument.

15 Press both indentations of the Tip Container to take the Tip Container out of the instrument.

NOTE

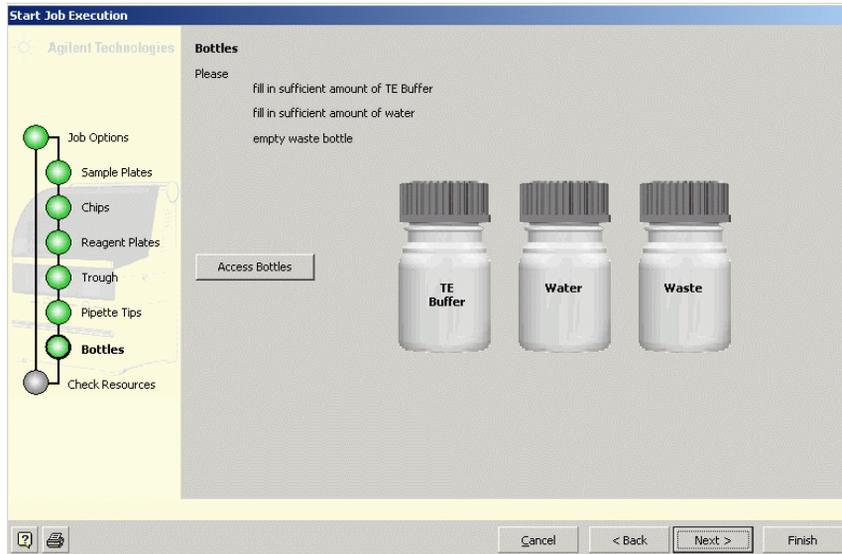
Remove all tips that were left in the instrument. Always start filling of the tip container with new tips from position A1.

16 The number and position of tips that have to be inserted is displayed on the screen of the Start Execution dialog. Position A1 is at the lower left corner of the displayed Tip Container.

17 Insert new tips and plug the tip container into the receptacle of the plate handler.

18 Click on *Close Left Door* button.

19 Click *Next* to proceed with the Job Start execution dialog.



20 Click *Access Bottles* to unlock the front cover of the instrument and open it.

NOTE

Four bottles are currently used by the instrument, whereas the display shows three bottles.

21 Pour the total volume of the Washing Solution (Reagent Kit) into the small left hand bottle.

22 Fill up the large water bottle with water.

23 Empty the large waste bottle.

CAUTION

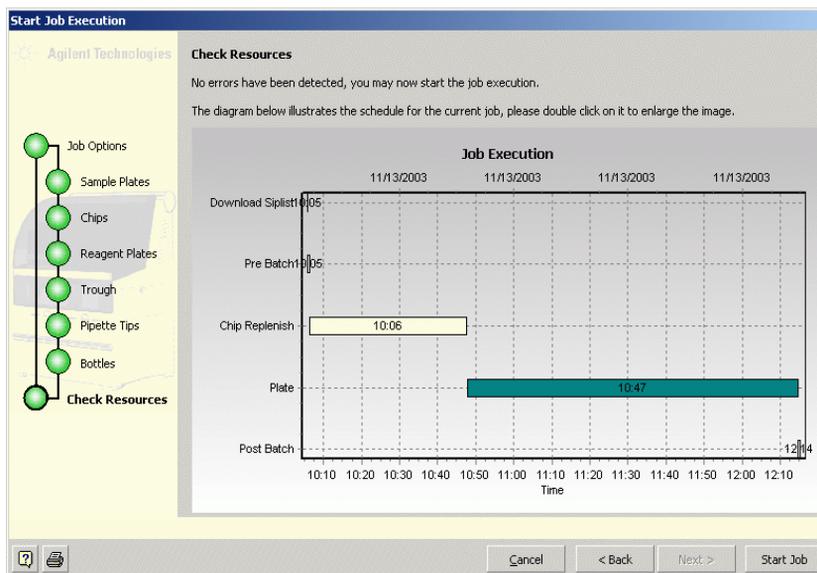
Carefully close all bottles. Unclosed bottles may lead to an insufficient chip replenishment.

24 Carefully close the front cover of the instrument.

NOTE

Orange light must be turned off.

25 Click *Next* to proceed with the Job Start execution dialog.



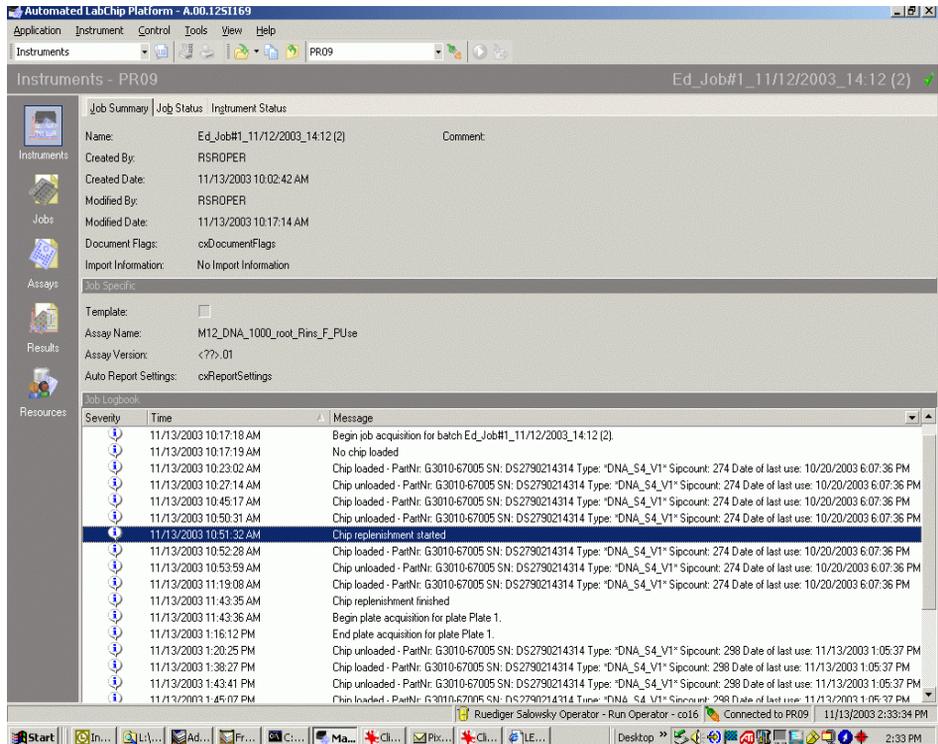
26 The appearing diagram illustrates the calculated schedule for the current job. Click *Start Job* to execute the current job.

Job Execution

During job execution information is available on three levels of the software to check the status of the current job.

Job Summary

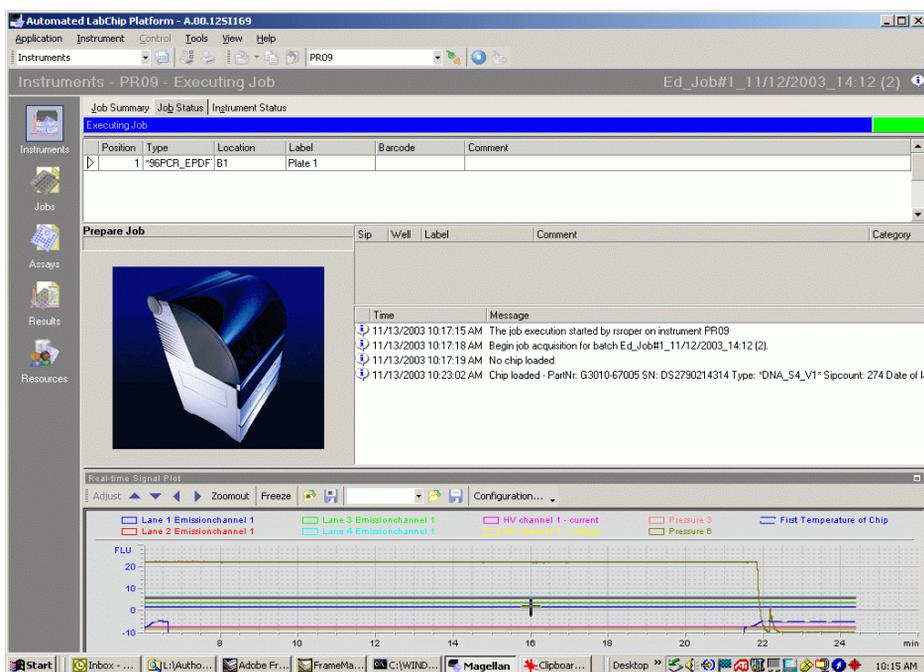
The Job Summary tab provides a general overview on Job name, - Creator, Creation date and assay name. All major events generated by the instrument are registered in the *Job Logbook* that will be consecutively filled during analysis.



Job Status

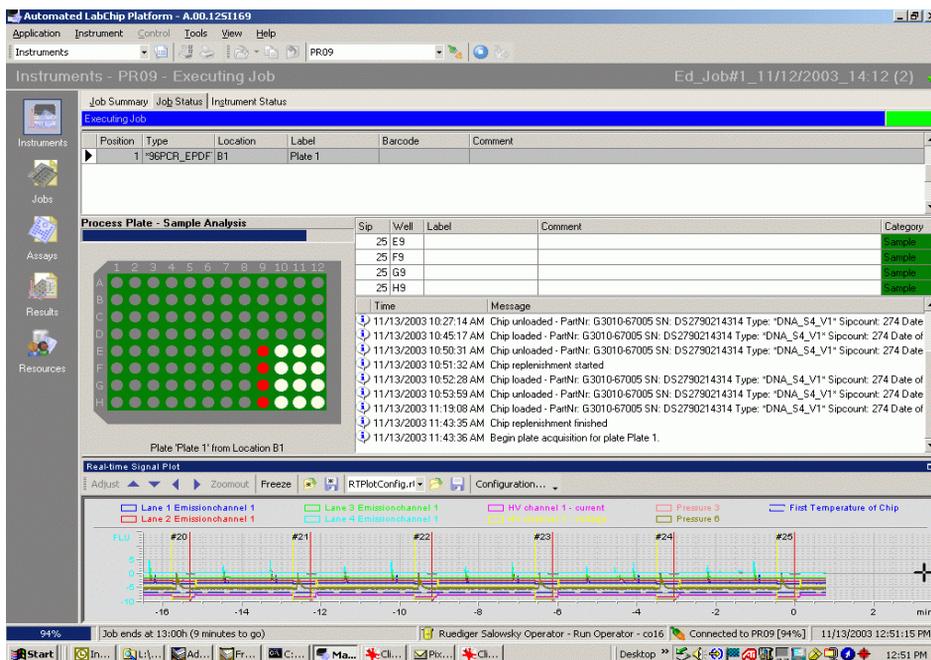
The *Job Status* tab is divided into several information panels. Information on the selected sample plates of the current job is displayed on the top of the tab. The Job Logbook appears in the middle of the screen next to the status display. The Real-time signal plot in the lower part of the screen displays the major incoming data acquired by the instrument.

1 Rinse Chip/Chip replenishment



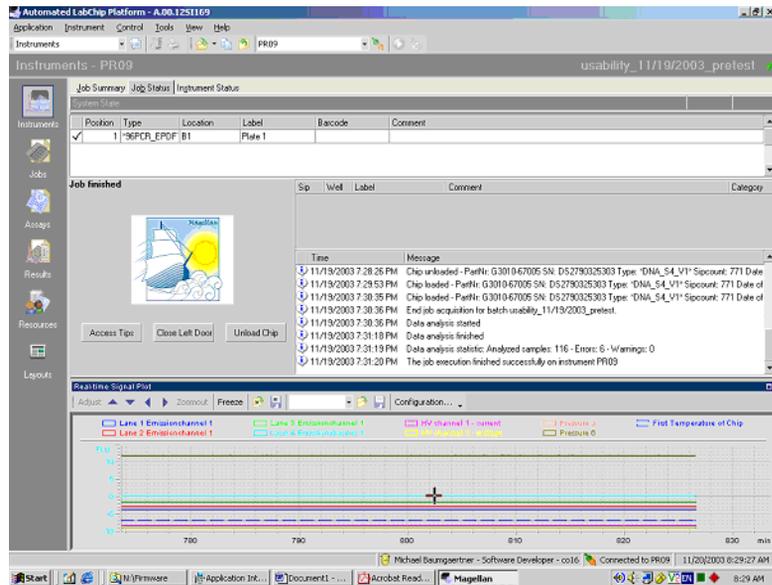
2 Sample analysis

During data acquisition the analyzed plate is shown on the status display indicating the wells on the plate that are currently processed. The name and position of the analyzed samples are displayed on the top of the logbook.



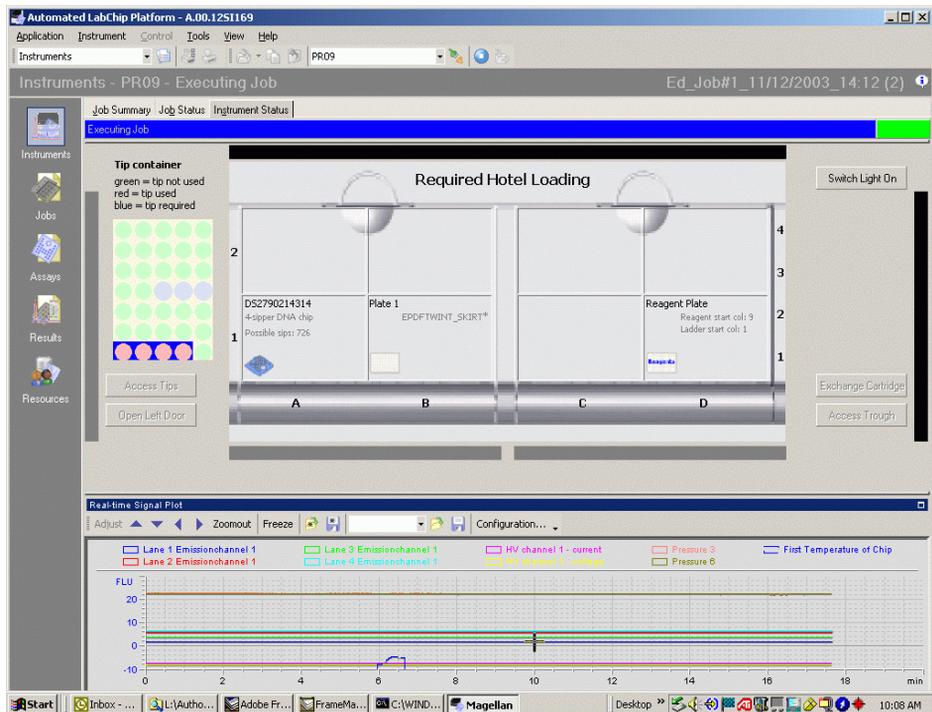
3 Job finished

The *Job Status* tab of a finished Job contains the complete Logbook as well as the Real-time Signal Plot.



Instrument Status

The Instrument Status tab displays the current Depot loading of the instrument as well as the Real-time signal plot. The status bar coloured in blue as well as the coloured rectangle in the upper right corner (green = active instrument status/red = error status) provide information on the current instrument state.



Finalizing a job

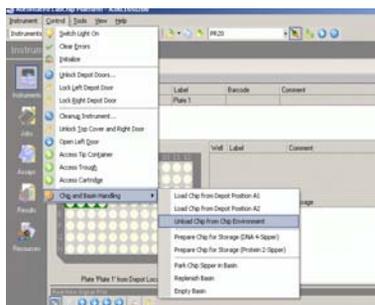
- 1 Close job in the instrument context

NOTE

After execution of the job the chip will be stored in the chip environment of the instrument.

Instrument clean up

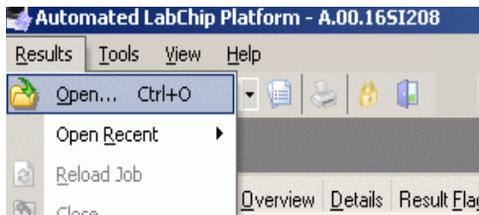
- 1 Select Control Menu Bar click on *Chip and Basin Handling>Unload Chip from Chip Environment* to transfer the chip from the chip environment to the designated rack in the instrument depot.



- 2 Open the front door of the depot and take out the rack with the chip.
- 3 Carefully insert the chip into the Chip box and store it at 4°C.
- 4 Empty the waste bottle.
- 5 Remove the sample and reagent plates from the depot and store them at 4°C
- 6 Empty the tip container.

Result Review

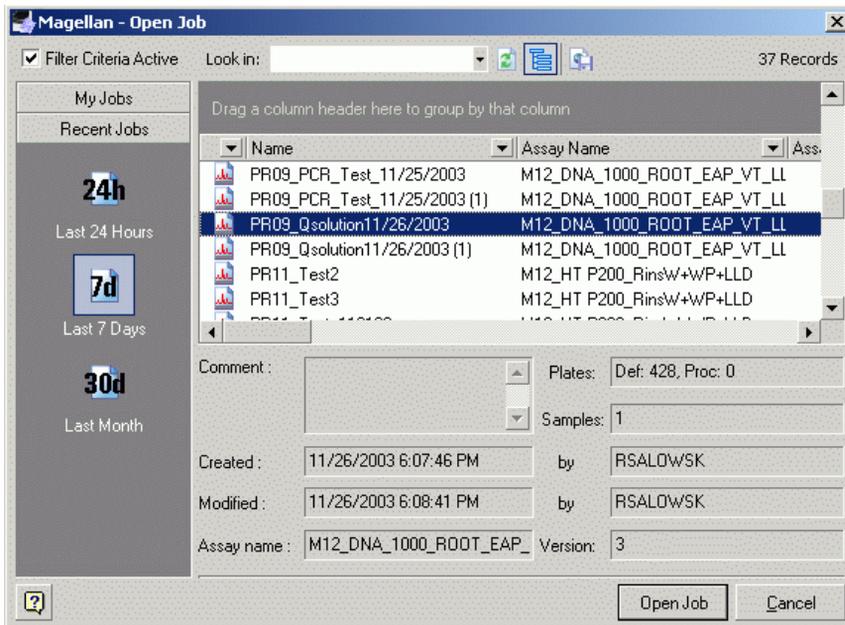
- 1 Click on the *Results* button on the Context toolbar to switch to the Result context. The Result context allows the analysis and review of the acquired data.
- 2 Go to *Results* and click on *Open...* or directly click on the *Open Job* button in the menu bar.



- 3 Select a Job in the database and click on *Open Job*.

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Result Review



NOTE

The Result context of the 5100 ALP software provides multifaceted options for analyzing, arranging and reviewing the acquired data. This guide will focus on the Graph and the Gel tab of the Details tab allowing to review the data either as an electropherogram or as gel-like image.

Details Tab

The Details tab is divided into two different information panels: Sample table and Sample Details.

The screenshot displays the 'Details' tab for 'Plate 1 (1), Unknown (E3)'. The 'Sample Table' lists the following data:

| Resu | Cate | Well | Sample Name | Comment | Stat |
|--------|------|------|-------------|---------|------|
| All... | S | E3 | Unknown | | ✓ |
| All... | S | F3 | Unknown | | ✓ |
| All... | S | F3 | Unknown | | ✓ |
| All... | S | G3 | Unknown | | ✓ |
| All... | S | G3 | Unknown | | ✓ |
| All... | S | H3 | Unknown | | ✓ |
| All... | S | H3 | Unknown | | ✓ |
| All... | S | A4 | Unknown | | ✓ |
| All... | S | A4 | Unknown | | ✓ |
| All... | S | B4 | Unknown | | ✓ |

The 'Details' section shows a 'Graph' of 'FU' vs 'Size (bp)'. Two peaks are identified: a 'Lower Marker' at 905 bp and an 'Upper Marker' at 1500 bp. The 'Standard' panel on the right contains the following settings:

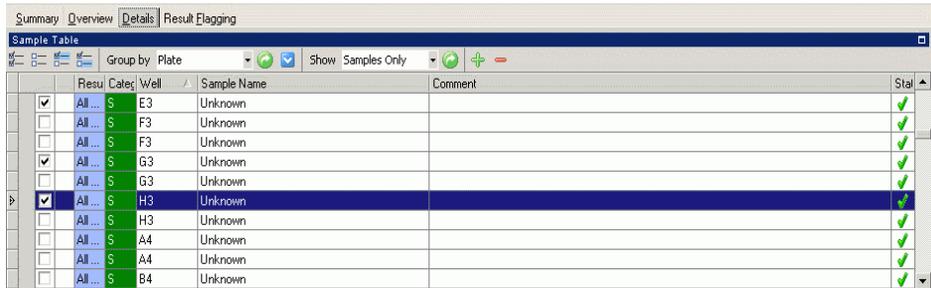
| Setting | Value |
|----------------------------------|-------------------------------------|
| Apply baseline removal | <input checked="" type="checkbox"/> |
| Apply smoothing | <input checked="" type="checkbox"/> |
| Height threshold (Abs) (Sample) | 0.40 |
| Area threshold (Sample)/Upper M | 0.00 |
| Width threshold (Sample)/Upper f | 0.20 |

Below the graph, a table provides further details for the markers:

| Channel | ID | Size [bp] | Concentration | Molarity | Observation |
|---------|----|-----------|---------------|----------|--------------|
| LM | 1 | | | | Lower Marker |
| S/UM | 1 | 905 | 14.0 | 23.4 | |
| S/UM | 2 | 1500 | 5.0 | 5.1 | Upper Marker |

1. Sample Table

The Sample Table allows the grouping of all sample measurements within the selected job and provides information on Sample Category, Samples Name, Analysis State, etc.



The screenshot shows a software interface with a 'Sample Table' window. The window has a title bar with 'Summary Overview Details Result Flagging' and a toolbar with icons for refresh, zoom, and other functions. Below the toolbar, there are controls for 'Group by Plate' and 'Show Samples Only'. The main area is a table with the following columns: Result, Category, Well, Sample Name, Comment, and Status. The table contains 10 rows of data, with the 6th row highlighted in blue. The Status column contains green checkmarks.

| | Result | Category | Well | Sample Name | Comment | Status |
|-------------------------------------|---------|----------|------|-------------|---------|--------|
| <input checked="" type="checkbox"/> | All ... | S | E3 | Unknown | | ✓ |
| <input type="checkbox"/> | All ... | S | F3 | Unknown | | ✓ |
| <input type="checkbox"/> | All ... | S | F3 | Unknown | | ✓ |
| <input checked="" type="checkbox"/> | All ... | S | G3 | Unknown | | ✓ |
| <input type="checkbox"/> | All ... | S | G3 | Unknown | | ✓ |
| <input checked="" type="checkbox"/> | All ... | S | H3 | Unknown | | ✓ |
| <input type="checkbox"/> | All ... | S | H3 | Unknown | | ✓ |
| <input type="checkbox"/> | All ... | S | A4 | Unknown | | ✓ |
| <input type="checkbox"/> | All ... | S | A4 | Unknown | | ✓ |
| <input type="checkbox"/> | All ... | S | B4 | Unknown | | ✓ |

2. Sample Details

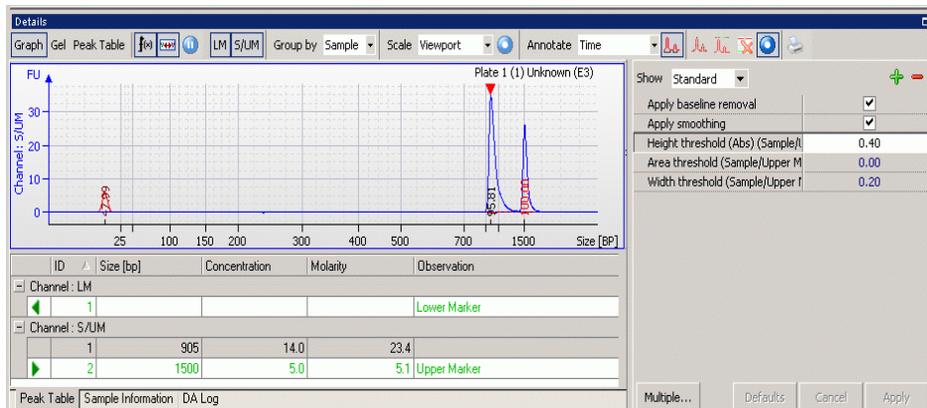
The Sample Details tab contains the Gel-, Graph-, and Peak Table tab providing all sample related informations. All sample related informations are shown on the lower left part of the display, whereas the Assay Setpoint Parameters are shown on the right as a flip chart.

The Graph Tab



The Graph Tab displays the acquired data as electropherograms and optional in the Peak Table the calculated values (fragment concentration, fragment size, molarity, etc.).

Click on sample row in the Sample Table to select a sample. The selected sample will be highlighted and displayed as an electropherogram in the Graph View



Further results are available in the a) Peak Table tab, b) Sample Information tab, and c) DA Log tab.

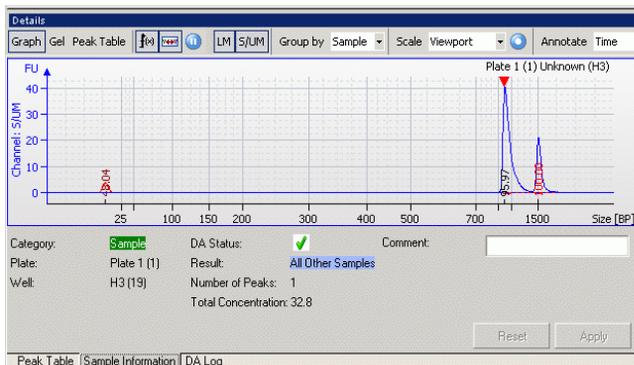
Peak table tab

The peak table tab contains peak related values (e.g. sample Size, Concentration, Molarity) calculated by the software.

| ID | Size [bp] | Concentration | Molarity | Observation |
|-----------------|-----------|---------------|----------|--------------|
| - Channel: LM | | | | |
| 1 | | | | Lower Marker |
| - Channel: S/UM | | | | |
| 1 | 905 | 14.0 | 23.4 | |
| 2 | 1500 | 5.0 | 5.1 | Upper Marker |

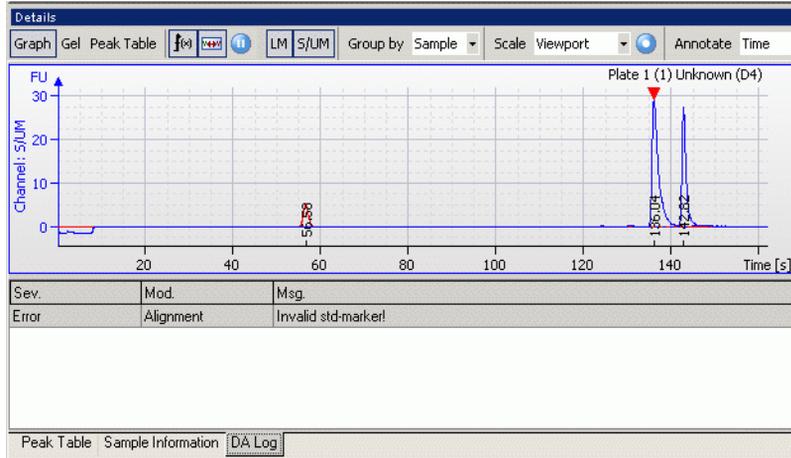
Sample Information tab

The Sample Information tab provide general informations on the analysis of each sample



DA Log tab

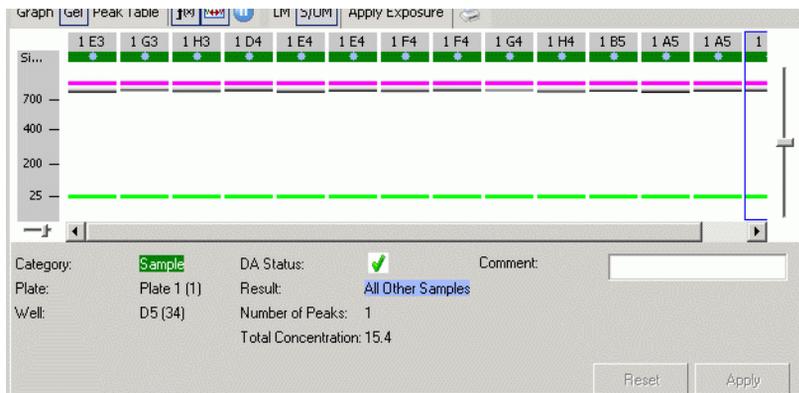
If data analysis of a focussed sample failed, the DA Log provides a short description of the failure.



The Gel Tab



The Gel Tab contains the Gel-like image and the a) Peak Table tab, b) Sample Information tab, and c) DA Log tab as in the Graph Tab.

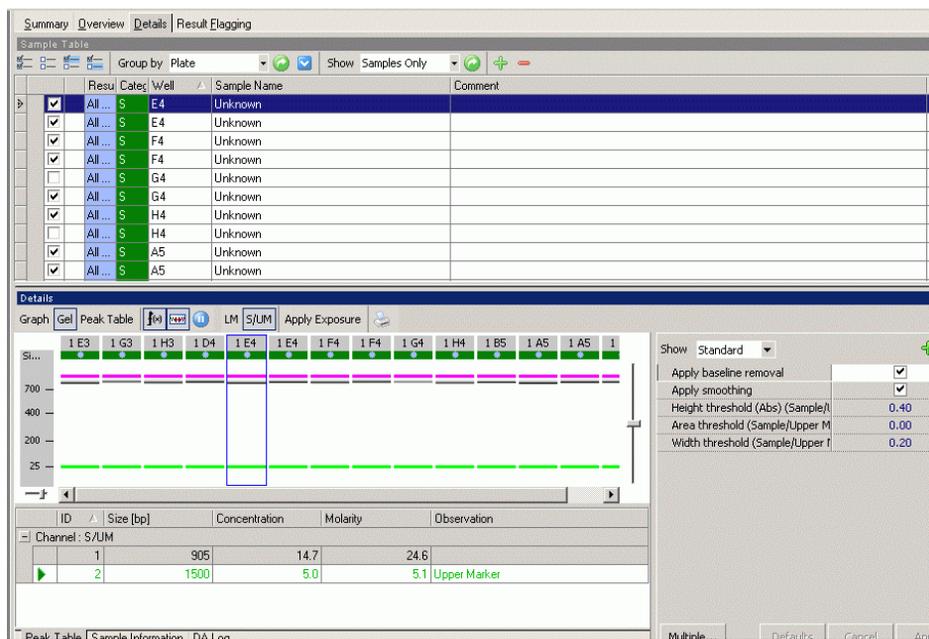


Reviewing Results in the Gel Tab

- 1 Check the samples in the Sample Table to show them in the Gel View.

NOTE

Only samples checked with a check mark on the left hand side of the Sample Table will be displayed in a gel-like image.



- 2 Double-click on a specific lane in the Gel-like image directly navigates to the associated electropherogram in the Graph Tab.

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Result Review

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